SUPPLEMENTARY DATA

FIG. S1. Maximum likelihood best-scoring topology obtained from the combined molecular dataset showing branch lengths (-ln likelihood = 30001). Tribes and major clades within Tigridieae, are labelled above the corresponding branches.
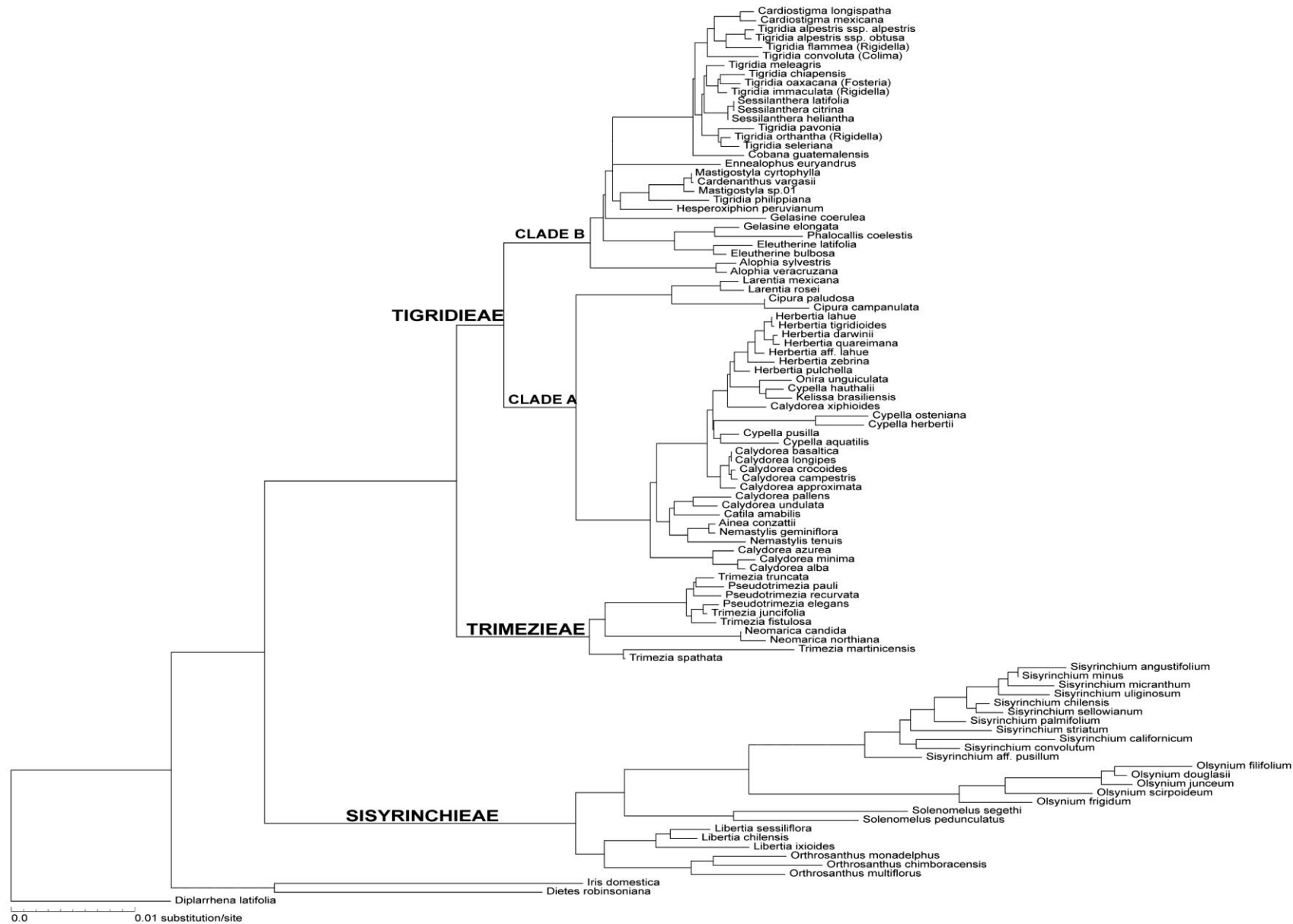
FIG. S2A. Trees showing the ML optimisation of the anatomical type (character A) of glandular structures on the ML best-scoring tree for the basal nodes of the three study tribes, and for Sisyrincheae and Trimezieae. Relative likelihoods corresponding to the likelihood values calculated for each character state are reported on nodes.
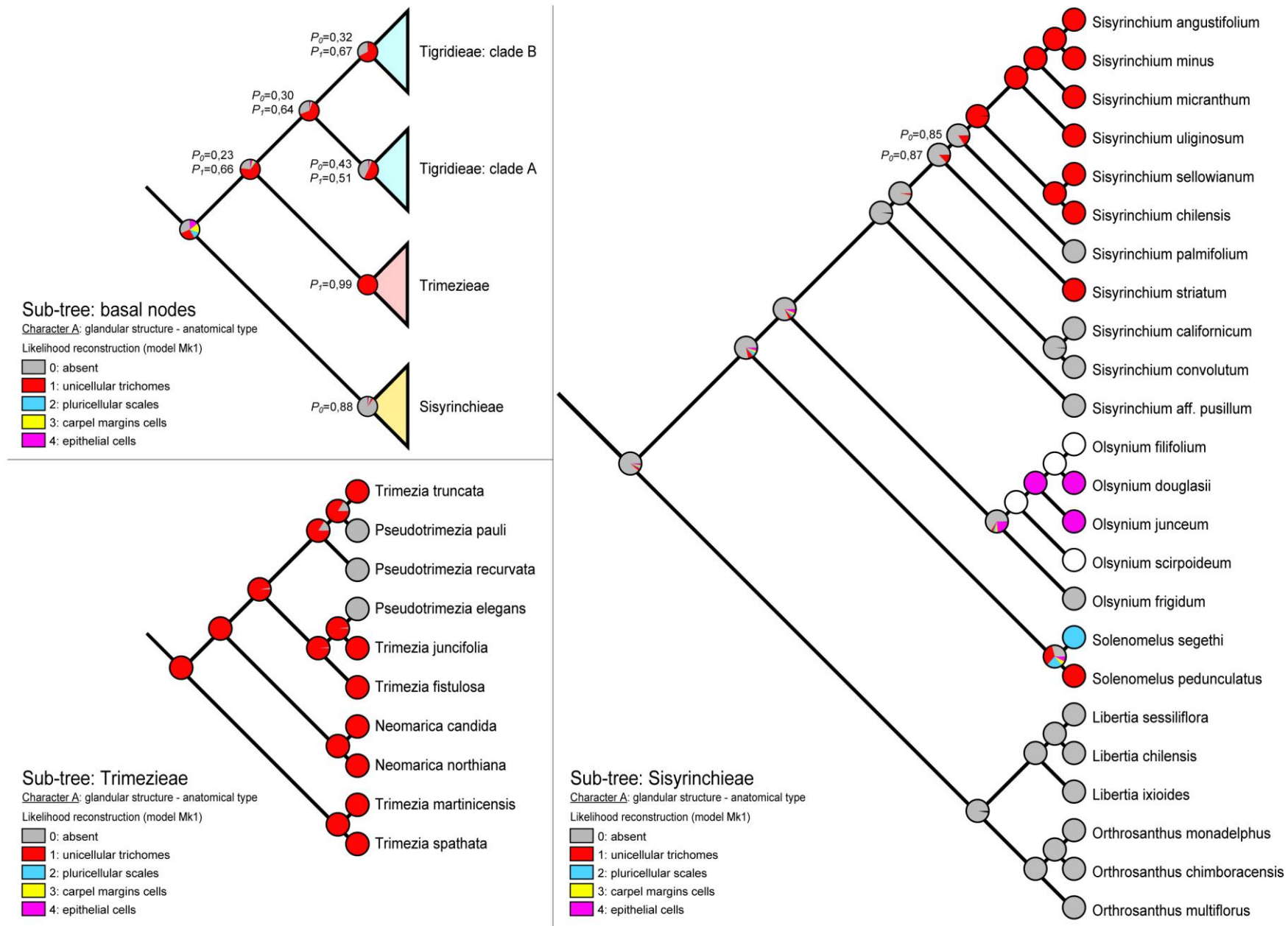
FIG. S2B. Trees showing the ML optimisation of the anatomical type (character A) of glandular structures on the ML best-scoring tree for clades A and B of Tigridieae. Relative likelihoods corresponding to the likelihood values calculated for each character state are reported on nodes.
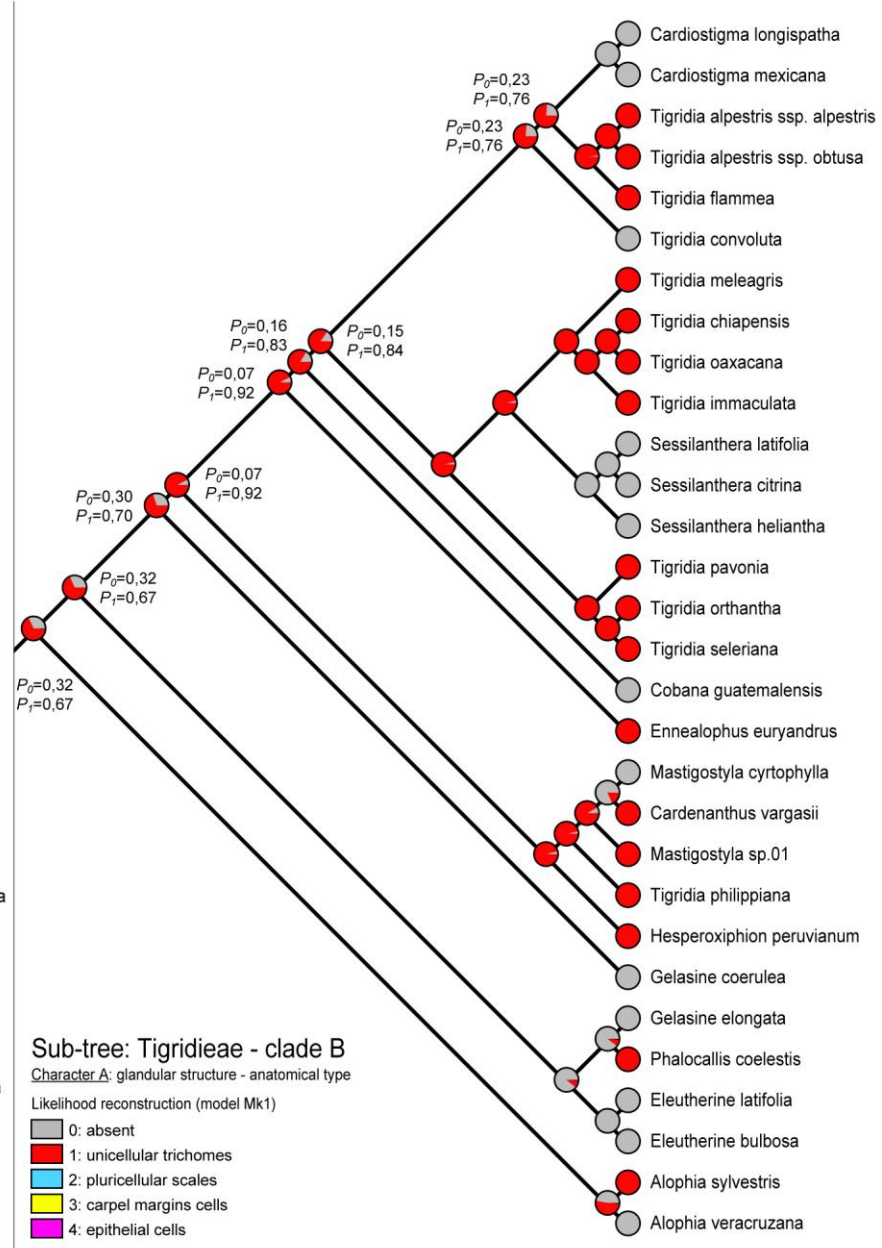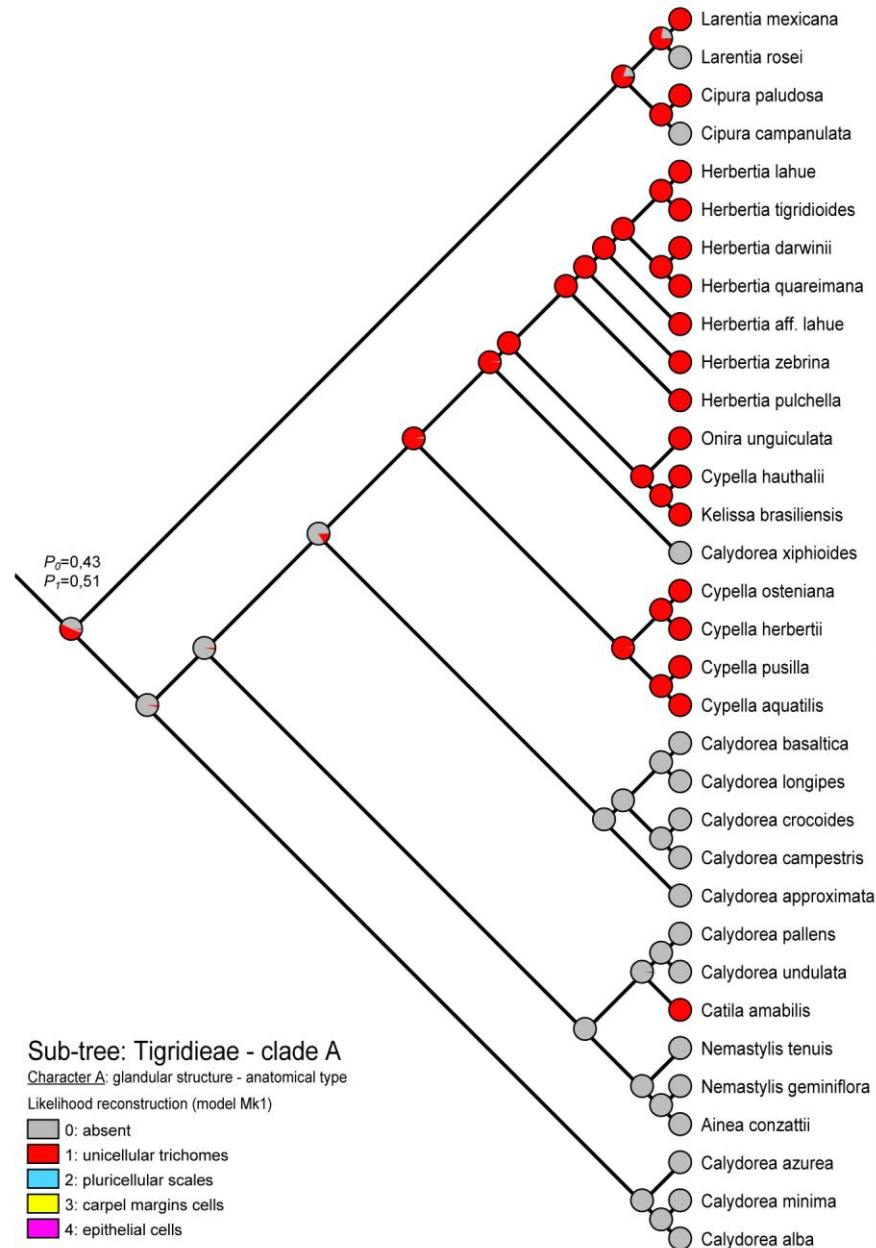
FIG. S3A. Trees showing the ML optimisation of the secretory type (character B) of glandular structures on the ML best-scoring tree for the basal nodes of the three study tribes, and for Sisyrinchieae and Trimezieae. Relative likelihoods corresponding to the likelihood values calculated for each character state are reported on nodes.
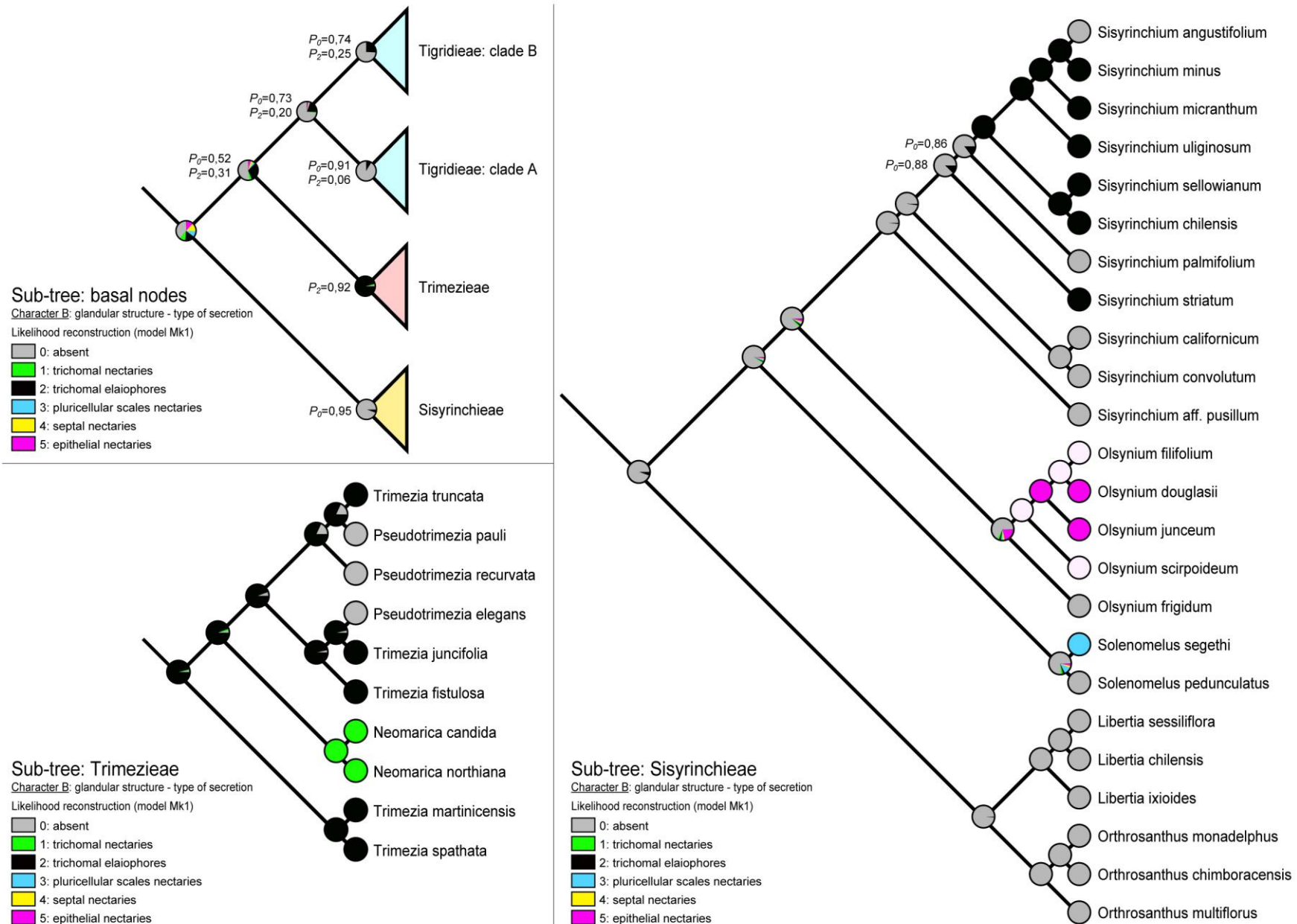
FIG. S3B. Trees showing the ML optimisation of the secretory type (character B) of glandular structures on the ML best-scoring tree for clades A and B of Tigridieae. Relative likelihoods corresponding to the likelihood values calculated for each character state are reported on nodes.

Sub-tree: Tigridieae - clade A

Character B: glandular structure - type of secretion

Likelihood reconstruction (model Mk1)
- 0: absent
- 1: trichomal nectaries
- 2: trichomal elaiophores
- 3: pluricellular scales nectaries
- 4: septal nectaries
- 5: epithelial nectaries

Sub-tree: Tigridieae - clade B

Character B: glandular structure - type of secretion

Likelihood reconstruction (model Mk1)
- 0: absent
- 1: trichomal nectaries
- 2: trichomal elaiophores
- 3: pluricellular scales nectaries
- 4: septal nectaries
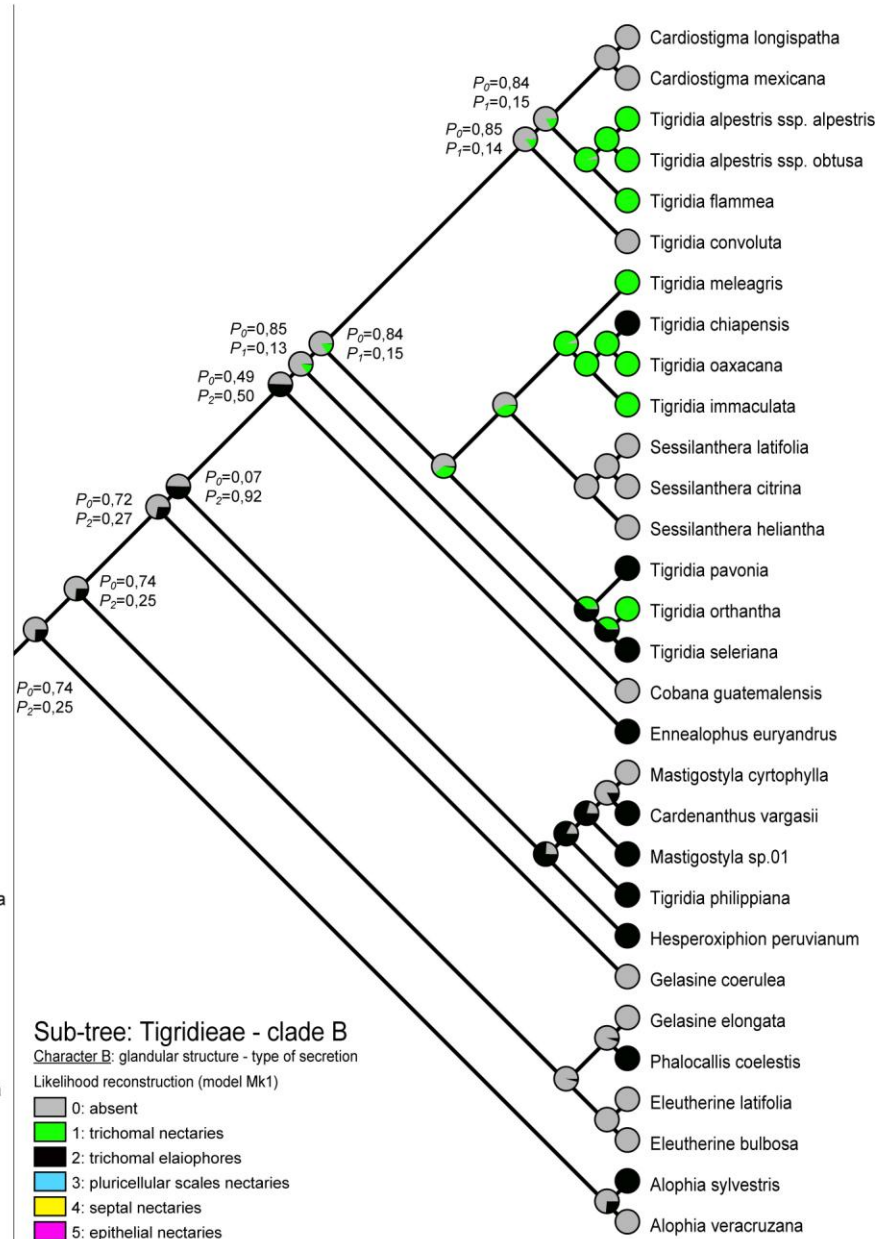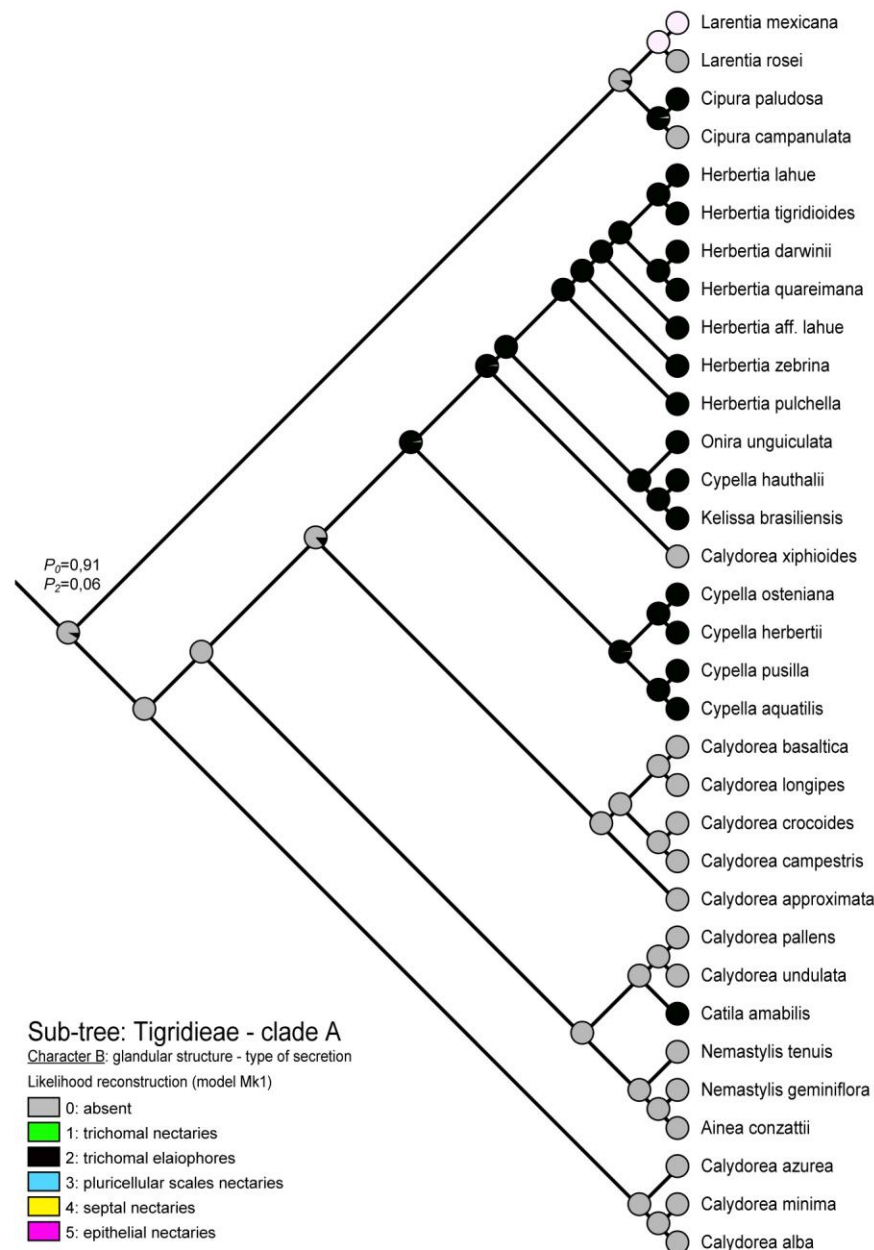- 5: epithelial nectaries

FIG. S4A. Trees showing the ML optimisation of the distribution (character C) of glandular structures within the flower on the ML best-scoring tree for the basal nodes of the three study tribes, and for Sisyrinchieae and Trimezieae. Relative likelihoods corresponding to the likelihood values calculated for each character state are reported on nodes.
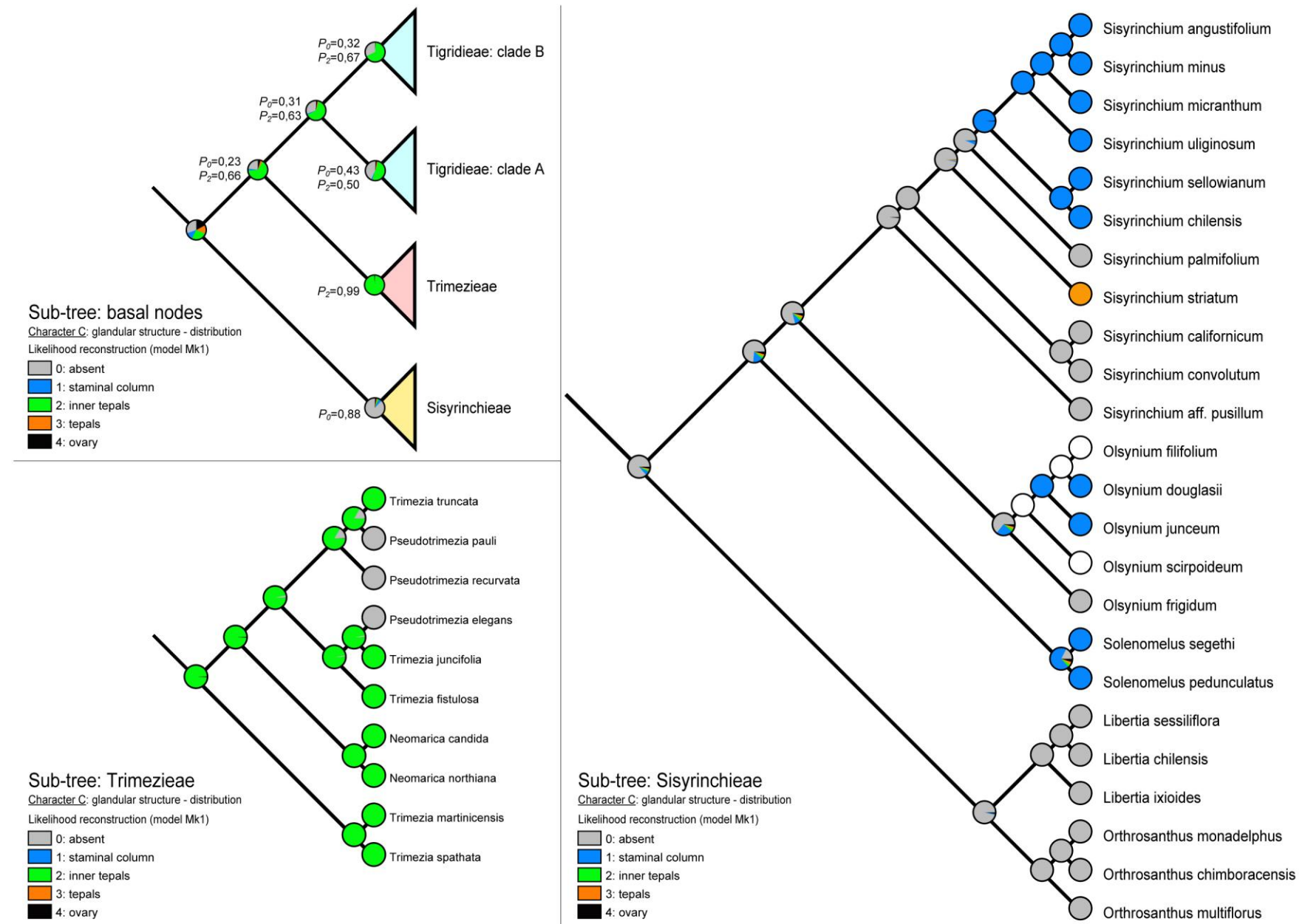
FIG. S4B. Trees showing the ML optimisation of the distribution (character C) of glandular structures within the flower on the ML best-scoring tree for clades A and B of Tigridieae. Relative likelihoods corresponding to the likelihood values calculated for each character state are reported on nodes.